

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
 An Unit _____ Phone Number 30 _____ Serial Number _____
 Mail Box and Bldg Room Location _____ Results Format Preferred circle PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Point of Contact:

Jan Delaval

Librarian

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>AW</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Quokka: Other _____
Date Searcher Reviewed: <u>12/19</u>	Bibliographic _____	Web Links _____
Date Completed: <u>12/19</u>	Citation _____	Indexing _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Client Prep Time: <u>10</u>	Patent Family _____	WWW/Internet _____
Final Time: <u>10</u>	Other _____	Other Special _____

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9	233	97.4	767	9	AX024687	Sequence
10	233	97.9	767	52	HSAB12834	Homo sapi
11	233	97.9	993	9	AX024689	Sequence
12	233	97.9	993	91	BC002843	Homo sapi
13	233	97.9	993	92	HSAB12835	Homo sapi
14	170	71.4	752	9	AX014787	Sequence
15	170	71.4	752	9	AX024691	Sequence
16	170	71.4	752	9	AX024693	Sequence
17	170	71.4	752	10	AX079857	Sequence
18	170	71.4	752	97	HSB97459	Human
19	170	71.4	755	9	AX042537	Sequence
20	170	71.4	755	92	HSAB03149	Homo sapi
21	170	71.4	806	88	AF038567	Homo sapi
22	170	71.1	873	93	U6237779	Homo sapi
23	170	71.4	2638	93	HSAB25977	Homo sapi
24	170	71.4	112874	78	AF277315	Homo sapi
25	23	10.1	217	9	AK312532	Sequence
26	26	8.1	21	9	AX024699	Sequence
27	26	8.1	52	9	AX351702	Sequence
28	26	8.1	21	19	AX079859	Sequence
29	20	8.4	1042	53	CNS0702A9	Brain
30	20	8.4	18414	76	AX079724	Brain
31	19	8.0	19	9	AP042534	Sequence
32	19	8.0	19	9	AP042539	Sequence
33	19	8.0	1838	10	U47665	Sequence
34	19	8.0	2941	8	X1085969	Xenopus lae
35	19	8.0	118429	79	AL158017	Homo sapi
36	19	8.0	127178	87	AC010490	Homo sapi
37	19	8.0	114677	61	AC009401	Homo sapi
38	19	8.0	160771	92	B595812	Human DNA
39	19	8.0	165228	85	AC005325	Homo sapi
40	19	8.0	172061	71	AC044114	Homo sapi
41	19	8.0	176092	74	AC073252	Homo sapi
42	19	8.0	1911144	90	AL365444	Human DNA
43	19	8.0	183196	76	AC083924	Homo sapi
44	19	8.0	184477	70	AC026272	Homo sapi
45	19	8.0	185676	82	AL550138	Homo sapi
46	19	8.0	187691	80	AL359087	Homo sapi
47	19	8.0	188776	70	AC026547	Homo sapi
48	19	8.0	212390	80	AL156377	Homo sapi
49	18	7.6	1997	94	U02906	Mus musculus
50	18	7.6	3010	98	XM189593	Xenopus lae

ALIGNMENT

RESULTS	1
AR042535	
Locus	192 kF TNA PAT 79 SEP 1999
DEFINITION	Sequence 4 from patent US 5811519.
ACCESSION	AR042535
VERSION	AR042535.1 GI:5963031
KEYWORDS	.
SOURCE	unknown.
ORGANISM	unknown
REFERENCE	Unclassified.
AUTHORS	1 (Eusebio, 1992)
TITLE	Lethe B ₂ , locus S ₁ . De Smets et al., Genebank.org and Euro-Flatbeat J
JOURNAL	(t)-l tumor specific genes
FEATURES	Patent: US 5811519-A 4 22 SEP 1999;
source	1. 1002 Organism="unknown"
BASE COUNT	179 a 302 c 336 g 185 t
ORIGIN	

```

Query Match      100.0%; Score 238; LR 9; Length 1002;
Best Local Similarity 100.0%; Pred. No. Ac-140;
Matches 238; Conservative 0; Mismatches 0; Models 0; Gaps 0;

```


P1 Room-Fallieur T, De Smet C, Godelaine D, Lothe B;
 P2 Lucas S;
 XX
 DR WPI: 1998-427951/36;
 DR P-PSDB: AAW69663;
 XX
 P1 New isolated LAGE-1 tumour associated nucleic acids caused to
 P2 develop products for the diagnosis and treatment of LAGE-1
 P3 associated disorders, particularly tumours;
 XX
 PS Claim 1: Page 60-62; 7pp; English;
 XX
 CC The present sequence encodes LAGE-1 tumour associated protein (LAP).
 CC The present invention also describes: (1) a method for treating a
 CC subject with a disorder characterised by expression of a LAGE-1 nucleic
 CC acid molecule or an expression product, comprising administering to the
 CC subject autologous cytolytic T cells to ameliorate the disorder, where
 CC the cytolytic T cells are specific for complexes of an HLA molecule and
 CC a LAGE-1 IAP or an immunogenic fragment; (2) a method for treating a
 CC subject with a disorder characterised by expression of a LAGE-1 nucleic
 CC acid molecule or an expression product, comprising administering a
 CC LAGE-1 IAP or an immunogenic fragment to ameliorate the disorder; and
 CC (3) a method for selectively erasing a population of T cells with
 CC cytolytic T cells specific for a LAGE-1 IAP comprising contacting an
 CC isolated population of T cells with an agent presenting a complex of a
 CC LAGE IAP or an immunogenic fragment and a HLA presenting molecule to
 CC selectively erase the isolated population of T cells with the cytolytic
 CC T cells. The methods and products from the present invention can be used
 CC for the diagnosis and treatment of LAGE-1 associated disorders;
 XX
 S0 Sequence 1002 BP; 179 A; 402 C; 336 G; 185 T; 0 other;
 Query Match: 100.0%; Score 248; BB 19; Length 1002;
 Best Local Similarity: 100.0%; Pred. No. 248-114;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 caagttacatttgaatgaacacacagatgcttttaccctgtttttggtcagact 60
 TT
 Tb 756 cagcttttccctgttgatgagacacagatgcttttaccctgtttttggtcagact 815
 QY 61 cctcagagacacagatgcttttaccctgtttttggtcagact 129
 TT
 Tb 816 cctcagagacacagatgcttttaccctgtttttggtcagact 875
 QY 121 ctatggaatgcttcacacacagatgcttttaccctgtttttggtcagact 189
 TT
 Tb 876 ctatggaatgcttcacacacagatgcttttaccctgtttttggtcagact 935
 QY 191 gaaatgagatgcttcacacacagatgcttttaccctgtttttggtcagact 249
 TT
 Tb 936 gaaatgagatgcttcacacacagatgcttttaccctgtttttggtcagact 993
 RESULT 2
 AAW00149
 ID AAW00149 standard; cDNA; 679 BP;
 AC AAW00149;
 XX
 DE 31 JUL-2000 (first entry)
 XX
 DE Human CTL-recognised Antigen on MELANOMA (CAMEL) protein encoding cDNA;
 XX
 KW CAMEL: CTL-recognised Antigen on MELANOMA; cytolysis T lymphocyte; CTL;
 KW tumour-associated antigen; LAGE-1; NY ES-1; anticancer; melanoma; human;
 KW cancer; immunotherapy; immune response; ss;
 XX
 SS Homo sapiens.
 XX
 FH Key
 PS 5'UTR 1..9
 FT

P1 /*aa a
 P2 10..239
 P3 /*aa b
 P4 /product "human CAMEL protein"
 P5 /note "tumour-associated antigen"
 P6 3'UTR 340..679
 P7 /aa c
 P8 K 20020564 AL
 XX
 PS 27-APR-2000;
 XX
 PF 15-OCT-1999; 99WP-EL07832;
 XX
 PR 16-OCT-1998; 98EP-0119583;
 XX
 PA (BIOH) ROCHERRECHER PROBLEME INT 0888;
 PA (OYR) UNIV HOSPITAL REIDER;
 XX
 PI Schröter FJ, Aarnoudse CA, Reider A, Klade C;
 XX WPI: 2000-339685/29;
 P2 P-PSDB: AAW70854;
 XX
 CC Tumour associated antigen useful for cancer immunotherapy is encoded by
 CC the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA;
 PS Claim 12: Page 54; 7pp; English;
 XX
 CC The present sequence is the 488 cDNA clone of a tumour-associated antigen
 CC CAMEL (Cytotoxic T lymphocytes (CTL) recognised Antigen on MELANOMA). It
 CC is encoded by the open reading frame (ORF-1 of LAGE-1 gene), a tumor-
 CC specific antigen. The 488 cDNA clone lacks the first 84 bp of the LAGE-1
 CC cDNA and shows strong homology with NY-ESO-1, a melanoma-specific tumour
 CC antigen. The tumour-associated antigen displayed on melanoma cells is
 CC recognised by cytotoxic T lymphocytes. CAMEL is expressed in tumour cell
 CC lines, tumour tissues (e.g. breast and lung) and in testicular number of
 CC healthy tissues. This sequence has anticancer activity. CAMEL tumour
 CC antigen and immunogenic peptides derived from it are useful for cancer
 CC immunotherapy. They have the potential to induce an immune response, by
 CC eliciting a CTL response. The cDNA molecule is used for construction of
 CC recombinant or fusion proteins.
 XX
 S0 Sequence 679 BP; 120 A; 208 C; 241 G; 140 T; 0 other;
 Query Match: 97.9%; Score 222; BB 21; Length 679;
 Best Local Similarity: 100.0%; Pred. No. 240-111;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 cagcttttccctgttgatgagacacagatgcttttaccctgtttttggtcagact 60
 TT
 Tb 432 cagcttttccctgttgatgagacacagatgcttttaccctgtttttggtcagact 490
 QY 61 cctcagagacacagatgcttttaccctgtttttggtcagact 129
 TT
 Tb 492 cctcagagacacagatgcttttaccctgtttttggtcagact 550
 QY 121 ctatggaatgcttcacacacagatgcttttaccctgtttttggtcagact 189
 TT
 Tb 552 ctatggaatgcttcacacacagatgcttttaccctgtttttggtcagact 610
 QY 191 gaaatgagatgcttcacacacagatgcttttaccctgtttttggtcagact 249
 TT
 Tb 612 gaaatgagatgcttcacacacagatgcttttaccctgtttttggtcagact 670
 RESULT 3
 AAW50447
 ID AAW50447 standard; cDNA; 755 BP;
 XX
 AC AAW50447;
 XX

DD	AAZ48482 standard; DNA: 52 bp.
XX	
AA'	AAZ48482;
XX	
DI	15-FEB-2000 (first entry)
XX	
FE	Human tumour antigen NY-ESO-1 reverse transcriptase cDNA product
XX	
XX	Cancer; Tumour; Antigen; MHC; major histocompatibility complex; T-cell; cytotoxic; helper; stimulation; proliferation; T-regulatory; diagnosis; prevention; melanoma; breast cancer; carcinoma; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma; reverse transcriptase; HIV; Kaposi's sarcoma;
ES	Synthetic.
OS	Homo Sapiens.
XX	
W	M0956548 AL.
XX	
DD	28-oct-1999.
XX	
PT	24-MAR-1999; 99WJ050687%.
XX	
PR	17 APR 1998; 98US002422.
ER	02-oct-1998; 98US016554%.
XX	
PA	(LJRW) LJRWG INS CANCER RES.
XX	
ST	Stockert E., Zander E., Chen Y., Stauden M., Alexander K., Hill Gué A., Ritter G.
XX	
DR	WPI: 2000-0408704.
XX	
PT	Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes
XX	
PS	Example 6; Page 13; 4pp; English.
XX	
CC	This sequence represents NY-ESO-1 reverse transcriptase cDNA (c11b) primer # 6, used with primer # 2 (AAZ48482) in studies to determine whether RNAs encoding the human tumour antigen NY-ESO-1 were expressed in melanoma cell lines and tumour samples. These localisation studies also revealed it to be expressed at high levels in normal ovary and testis, but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in culture supernatant and tumour cell lines with some degree of frequency; those included the melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. Peptides derived from NY-ESO-1 are bound by both MHC (major histocompatibility complex) class I and class II molecules, and presentation to T-cells. Peptides AAAY243Y2434 bind to class I and II molecules, thereby stimulating proliferation of cytotoxic T cells, whereas peptides AAAY243Y24349 bind to class II HLA DR53 molecules, stimulating helper T-cell proliferation. The peptides described in NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells
XX	
SS	Sequence: 52 BP; 6 A; 12 C; 7 G; 7 T; 6 other;
Query Match 8.4%, Score 20; Identity 100%; Length 52	
Best Local Similarity 100.00%; Pred. No. of gaps	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps	
DY	65 Complementarity 84
DE	52 AAAGAGAGAGAGTAAGAT 14
RSLI	20
AAP	50056%

Query Match: 8.4%; Score 20; LB 21; Length 42;
 Best local similarity: 100.0%; Pred. No. 9,52;
 Matches 20; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

 65 ccccccccccgcctacacc 84
 |||||c|||c|||c|||c|||
 42 CAGGGACAGGCGTAAAGC 14

 SHL 16
 Z4-1797
 AAZ49179 Standard; DNA: 42 bp.
 AAZ49179:

 14 APR 2000 (first entry)
 PCR primer for NY-ESO-1 coding sequence.

 SSX-2: SSX-2 gene; breast cancer metastasis; NY ESO-1; SEQ ID: NAME 4;
 diagnostic detection; tumour rejection and open precursor; PCR primer; SS.
 Homo sapiens

 WU200000042 AL.

 06 JAN 2000.
 03 JUN 1999: 99W0 US12293,
 26 JUN 1998: 96US-0105907,
 (UBM) LUDWIG INSI CANCER RES.,
 Sahlin U, Torrelvi, Chen Y, Old LJ, Pfreundschuh M;
 WPI: 2000 147070/12.

 detecting breast cancer and melanoma used for diagnosis and in
 development of targeted therapy .

 claim B; Page 5; 24pp; English.

 This sequence represents a PCR primer for the NY-ESO-1 gene.
 The invention relates to a method for determining breast cancer or
 melanoma in a sample by assaying for expression of a specific NY ESO-1, SSX-2 and
 SSX-4 for breast cancer, or NY-ESO-1, SSX-2 and MAXI-3 for melanoma, the
 expression of at least one is an indicator of possible breast cancer, and
 the expression of at least two is an indicator of possible melanoma. The
 method is used to diagnose breast cancer and melanoma, and to develop
 therapies, e.g. a mixture of peptides, derived from hetero and homo
 known to associate with major histocompatibility complex to promote
 cytolytic T-cell proliferation, can be prepared based on the determined
 pattern of antigen expression in a particular sample, containing two or
 more of the specified tumour rejection and open precursors improves the
 accuracy of the assay.

 Sequence: 42 bp; 6 A; 12 C; 7 G; 7 T; 0 other;

 Query Match: 8.4%; Score 20; LB 21; Length 42;
 Best local similarity: 100.0%; Pred. No. 9,52;
 Matches 20; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

 65 ccccccccccgcctacacc 84
 |||||c|||c|||c|||c|||
 42 CAGGGACAGGCGTAAAGC 14

 SHL 16
 Z4-1797

CLASSIFICATION:

1 ANTI SENSE: NO
2 ORIGINAL SOURCE:
3 ORGANISM: HOMO SAPIENS
4 FEATURE:
5 NAME/KEY: CUS
6 LOCATION: 102..809
7
8 US 08 265 087 4/0

Query Match 7.1% Score 17: 14 15 Length 1449

Best Local Similarity 100.0% Prod. No. 5.4

Matches 17: Conserved 0; Mismatches 0; Indels 0; Gaps 0

97 192 actacatattttttttt 208
106 1165 GTTAAAGTGGTGGTGGT 1149
1111111111111111

RESULT 19
US 08 265 087 4/0
Sequence 5, Application US/08/65097
Patent No. 571615

GENERAL INFORMATION:

1 APPLICANT: SCOTT, PHILIP
2 TITLE OF INVENTION: Compositions and Methods for Use of
3 FILE OF INVENTION: 11.12 as an Applicant
4 NUMBER OF SEQUENCES: 4
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Bowman and Bowson
7 STREET: Spring House
8 CITY: Spring House
9 STATE: Pennsylvania
10 COUNTRY: USA
11 ZIP: 19477

COMPUTER READABLE FORM:

1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC DOS/MS DOS
4 SOFTWARE: Patent In Release #1.0, Version #1.25
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/65097
7 FILING DATE:
8 CLASSIFICATION: 424

PRIOR APPLICATION DATA:

1 APPLICATION NUMBER: US/08/229,282

2 FILING DATE: 18 APR 1994

3 ATTORNEY/AGENT INFORMATION:

1 NAME: Bak, Mary E.

2 REGISTRATION NUMBER: 41,215

3 REFERENCE/WORK NUMBER: WST/USA

4 TELECOMMUNICATION INFORMATION:

1 TELEPHONE: 215-540-9206

2 TELEFAX: 215-540-9818

3 INFORMATION FOR SEQ ID NO: 4:

1 SEQUENCE CHARACTERISTICS:

1 LENGTH: 104 base pairs

2 TYPE: nucleic acid

3 STRANDEDNESS: double

4 TOPOLOGY: unknown

5 MOLECULE TYPE: cDNA

6 FEATURE:

1 NAME/KEY: CUS

2 LOCATION: 101..809

3
4 US 08 265 087 4

Query Match 7.1% Score 17: 14 15 Length 1449

Best Local Similarity 100.0% Prod. No. 5.4

Matches 17: Conserved 0; Mismatches 0; Indels 0; Gaps 0

97 192 actacatattttttttt 208
106 1165 GTTAAAGTGGTGGTGGT 1149
1111111111111111

106 1165 GTTAAAGTGGTGGTGGT 1149

RESULT 20

US 08 265 087 4/0
Sequence 5, Application US/08/62149
Patent No. 5725127

GENERAL INFORMATION:

1 APPLICANT: SCOTT, PHILIP
2 TITLE OF INVENTION: Compositions and Methods for Use of
3 FILE OF INVENTION: 11.12 as an Applicant
4 NUMBER OF SEQUENCES: 4
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Bowman and Bowson
7 STREET: Spring House Corporate Center, P.O. Box 19
8 CITY: Spring House
9 STATE: Pennsylvania
10 COUNTRY: USA
11 ZIP: 19477

COMPUTER READABLE FORM:

1 MEDIUM TYPE: Floppy disk

2 COMPUTER: IBM PC compatible

3 OPERATING SYSTEM: PC DOS/MS DOS

4 SOFTWARE: Patent In Release #1.0, Version #1.25

5 CURRENT APPLICATION DATA:

1 APPLICATION NUMBER: 08/229,282

2 FILING DATE: 25 MAR 1994

3 CLASSIFICATION: 424

4 PRIOR APPLICATION DATA:

1 APPLICATION NUMBER: 08/229,282

2 FILING DATE: 17 JUN 1994

3 ATTORNEY/AGENT INFORMATION:

1 TELEPHONE: 215-540-9206

2 TELEFAX: 215-540-9818

3 INFORMATION FOR SEQ ID NO: 4:

1 SEQUENCE CHARACTERISTICS:

1 LENGTH: 104 base pairs

2 TYPE: nucleic acid

3 STRANDEDNESS: double

4 TOPOLOGY: unknown

5 MOLECULE TYPE: cDNA

6 FEATURE:

1 NAME/KEY: CUS

2 LOCATION: 101..809

3
4 US 08 621 494 4

Query Match 7.1% Score 17: 14 15 Length 1449

Best Local Similarity 100.0% Prod. No. 5.4

Matches 17: Conserved 0; Mismatches 0; Indels 0; Gaps 0

97 192 actacatattttttttt 208

106 1165 GTTAAAGTGGTGGTGGT 1149

1111111111111111

RESULT 21

US 08 265 087 4/0
Sequence 5, Application US/08/65098
Patent No. 5725127

GENERAL INFORMATION:

1 APPLICANT: SCOTT, PHILIP
2 TITLE OF INVENTION: Compositions and Methods for Use of
3 FILE OF INVENTION: 11.12 as an Applicant
4 NUMBER OF SEQUENCES: 4


```

1  APPLICATION NUMBER: JPL 226270
2  FILING DATE: 21 SEPT 1994
3  APPLICATION NUMBER: PCT/JP95/00160
4  FILING DATE: 21 SEPT 1995
5  ATTORNEY/AGENT INFORMATION:
6  NAME: Tetsuo F. Chapman
7  REGISTRATION NUMBER: 42549
8  REFERENCE/INVENTOR NUMBER: P0997 Case 144
9  TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (616) 861-1156
11 TELEFAX: (616) 861-5465
12 INFORMATION FOR SEQ ID NO: 1:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 1688
15 TYPE: nucleic acid
16 STRANDEDNESS: double
17 TOPOLOGY: linear
18 MOLECULE TYPE: cDNA to mRNA
19 ORIGINAL SOURCE:
20 ORGANISM: Homo sapiens
21 US 08 649 619B 2
22
23 Query Match
24 Best Local Similarity: 100.0% Freq. No. 5, 42
25 Matches: 17; Conservation: 0; Mismatches: 0; Indels: 0; Gaps: 0
26
27 85 conserved sequence 101
28
29 453 CAGAGTGGAGGAGGCTTTC 279
30
31 RESULT 25
32 PCT US94 12883 4
33 Sequence 4: Application PCT/JP94 12883
34 GENERAL INFORMATION:
35 TITLE OF INVENTION: OBLIGATORY NUCLEAR RECEPTOR COMPLEXES AND
36 TITLE OF INVENTION: METHODS
37 NUMBER OF SEQUENCES: 48
38 CORRESPONDENCE ADDRESS:
39 ADDRESSEE: Arnold, White & Burke
40 STREET: P.O. Box 4433
41 CITY: Houston
42 STATE: Texas
43 COUNTRY: United States of America
44 ZIP: 77240
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: floppy disk
47 COMPUTER: IBM pc compatible
48 OPERATING SYSTEM: PC DOS/MS-DOS/Windows
49 SOFTWARE: Patent In Release #1.0, Version
50
51 CURRENT APPLICATION DATA:
52 APPLICATION NUMBER: PCT/JP94/12883
53 FILING DATE: Concurrently herewith
54 CLASSIFICATION:
55 PRIOR APPLICATION DATA:
56 APPLICATION NUMBER: US 08/152,363
57 FILING DATE: 10 NOV 1994
58 CLASSIFICATION:
59 ATTORNEY/AGENT INFORMATION:
60 NAME: BARBARA S. KILHELL
61 REGISTRATION NUMBER: 43,928
62 REFERENCE/INVENTOR NUMBER: APT 0144P
63 TELECOMMUNICATION INFORMATION:
64 TELEPHONE: (512) 418-5000
65 TELEFAX: (512) 789-2679
66 TELEX: 79 0924
67 INFORMATION FOR SEQ ID NO: 4:
68 SEQUENCE CHARACTERISTICS:
69 LENGTH: 1814 base pairs
70 TYPE: nucleic acid

```

```

1  STRANDEDNESS: single
2  TOPOLOGY: linear
3  MOLECULE TYPE: cDNA (genomic)
4  PCT US94 12883 5
5
6 Query Match
7 Best Local Similarity: 100.0% Freq. No. 5, 42
8 Matches: 17; Conservation: 0; Mismatches: 0; Indels: 0; Gaps: 0
9
10 85 conserved sequence 101
11
12 453 CAGAGTGGAGGAGGCTTTC 56
13
14 RESULT 25
15 US 08 649 619B 1
16 Sequence 1: Application US/08/649 198
17 Patent No. 5871916
18 GENERAL INFORMATION:
19 TITLE OF INVENTION: OBLIGATORY NUCLEAR RECEPTOR COMPLEXES AND
20 TITLE OF INVENTION: METHODS
21 NUMBER OF SEQUENCES: 11
22 CORRESPONDENCE ADDRESS:
23 ADDRESSEE: FLYNN, THELMA BOWHELL &
24 STREET: 2026 Randleman Road
25 CITY: Kalamazoo
26 STATE: Michigan
27 COUNTRY: USA
28 ZIP: 49008 1699
29 COMPUTER READABLE FORM:
30 MEDIUM TYPE: floppy disk
31 MEDIUM TYPE: storage
32 COMPUTER: IBM PC/AT compatible
33 OPERATING SYSTEM: MS DOS 5.0
34 SOFTWARE: WordPerfect 5.0
35
36 CURRENT APPLICATION DATA:
37 APPLICATION NUMBER: PCT/JP94/0144P
38 FILING DATE:
39 CLASSIFICATION: 435
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: JPL 226270
42 FILING DATE: 21 SEPT 1994
43 APPLICATION NUMBER: PCT/JP95/00160
44 FILING DATE: 21 SEPT 1995
45 ATTORNEY/AGENT INFORMATION:
46 NAME: Tetsuo F. Chapman
47 REGISTRATION NUMBER: 42549
48 REFERENCE/INVENTOR NUMBER: P0997 Case 144
49 TELECOMMUNICATION INFORMATION:
50 TELEPHONE: (616) 861-1156
51 TELEFAX: (616) 861-5465
52 INFORMATION FOR SEQ ID NO: 1:
53 SEQUENCE CHARACTERISTICS:
54 LENGTH: 1688
55 TYPE: nucleic acid
56 STRANDEDNESS: double
57 TOPOLOGY: linear
58 MOLECULE TYPE: cDNA to mRNA
59 ORIGINAL SOURCE:
60 ORGANISM: Homo sapiens
61 IMMEDIATE SOURCE:
62 LIBRARY: Human mammary gland cDNA
63 FEATURES:
64 NAME/KEY: cUS
65 LOCATION: 206...191
66 PCT/JP94 12883 4
67 US 08 649 619B 1

```

Query Match 7.14; Score 17; DB 2; Length 1979;
Best Local Similarity 100.0%; Prod. No. 5.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 caagctagagcccttc 101
|||||
DB 264 caagctagagcccttc 279

Search completed: October 9, 2001, 15:36:04
Job time: 2824 sec

GenCore version 4.5
Copyright (c) 1993-2000 Compugen Ltd.

OM nucleole nucleole search, using sw model

Run on: October 9, 2001, 14:02:40 : Search time 169.25 seconds
(without alignments)
1645.074 Million cell updates/sec

Files: US-09-341-829A-4_copy_756_993

Perfect score: 248

Sequence: 1 cagtttccctttatattatg.....aaatctaaatcagattccg 248

Scoring table: cdld95.NUP

Gapop 60.0 : Gapext 40.0

Searched: 16228115 seqs, 4726426750 residues

Word size: 0

Total number of hits satisfying chosen parameters: 20456240

Minimum DB seq length: 0

Maximum DB seq length: 2400000000

Post processing: listing first 50 summaries

Database:

ESL: *

44: em_est_hum16: *

45: em_est_hum17: *

46: em_est_hum18: *

47: em_est_hum19: *

48: em_est_hum20: *

49: em_est_hum21: *

50: em_est_hum22: *

51: em_est_hum23: *

52: em_est_hum24: *

53: em_est_hum25: *

54: em_est_hum26: *

55: em_est_hum27: *

56: em_est_hum28: *

57: em_est_hum29: *

58: em_est_hum30: *

59: em_est_hum31: *

60: em_est_hum32: *

61: em_est_hum33: *

62: em_est_hum34: *

63: em_est_hum35: *

64: em_est_hum36: *

65: em_est_hum37: *

66: em_est_hum38: *

67: em_est_hum39: *

68: em_est_hum40: *

69: em_est_hum41: *

70: em_est_hum42: *

71: em_est_hum43: *

72: em_est_hum44: *

73: em_est_hum45: *

74: em_est_hum46: *

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76: em_est_hum48: *

77: em_est_hum49: *

78: em_est_hum50: *

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81: em_est_hum53: *

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96: em_est_hum68: *

97: em_est_hum69: *

98: em_est_hum70: *

99: em_est_hum71: *

100: em_est_hum72: *

101: em_est_hum73: *

102: em_est_hum74: *

103: em_est_hum75: *

104: em_est_hum76: *

105: em_est_hum77: *

106: em_est_hum78: *

107: em_est_hum79: *

108: em_est_hum80: *

109: em_est_hum81: *

110: em_est_hum82: *

111: em_est_hum83: *

112: em_est_hum84: *

113: em_est_hum85: *

114: em_est_hum86: *

115: em_est_hum87: *

116: em_est_hum88: *

117: em_est_hum89: *

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117: qb_est148:*
118: qb_est49:*
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251: qb_est182:*
252: qb_est183:*
253: qb_est184:*
254: qb_est185:*
255: qb_est186:*
256: qb_est187:*
257: qb_est188:*
258: qb_est189:*

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Prod. No. is the number of results predicted by OLLIGO. The score is the score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

